

Amendments to the Specification:

Please replace the paragraph appearing at page 26, line 26 through page 27, line 3, with the following amended paragraph:

Each predicted ORF amino acid sequence was compared with all sequences found in current GENBANK, SWISS-PROT, and PIR databases using the BLAST algorithm. BLAST identifies local alignments occurring by chance between the ORF sequence and the sequence in the databank (~~Altschal~~ Altschul et al., 1990, E J Mol. Biol. 215:403-410). Homologous ORFs (probabilities less than  $10^{-5}$  by chance) ~~and ORF's~~ and ORF's that are probably non-homologous (probabilities greater than  $10^{-5}$  by chance) but have good codon usage were identified. Both homologous, sequences and non-homologous sequences with good codon usage, are likely to encode proteins and are encompassed by the invention.

Please replace the paragraph appearing at page 45, lines 1-11, with the following amended paragraph:

Homology searches can be performed using the BLAST algorithm contained in the Wisconsin Sequence Analysis Package (Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711) to compare each predicted ORF amino acid sequence with all sequences found in the current ~~GenBank~~ GENBANK, SWISS-PROT and PIR databases. BLAST searches for local alignments between the ORF and the databank sequences and reports a probability score which indicates the probability of finding this sequence by chance in the database. ORF's with significant homology (e.g. probabilities lower than  $1 \times 10^{-6}$  that the homology is only due to random chance) to membrane or exported proteins represent protein antigens for vaccine development. Possible functions can be provided to *M. catarrhalis* genes based on sequence homology to genes cloned in other organisms.